



## SEQUENCE LISTING

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<110> Fernandez, Elma  
Vernet, Corine  
Shimkets, Richard A.

<120> Novel Human Proteins and Polynucleotides Encoding Them

<130> Cura-46 (15966-546)

<140> USSN 09/544,511

<141> 2000-04-06

<150> USSN 60/128,514

<151> 1999-04-09

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<170> PatentIn Ver. 2.0

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21



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 agaaccaga acagaaggcc acaggtctggc actactgcat tctccttatg tgtctcaggc 4163  
 tgtggtgact ctacatggg catcgaagaa gtacaacca catagccctc tggagaccgc 4223  
 ctagatcaga gactcagcaa aaacaggtc gccttccctc tcccacatat gagtggaaact 4283  
 tacatgtgtc ctggtttgaa tgatcathtt gcaagccaca cgggttgga gaggtggtct 4343  
 caccacagac gtctttgcta atttgccac cttcacctac tgacatgacc aggattttcc 4403

tttgccatta aggaatgaac tctttcaagg agaggaaacc ctagactctg tgtcactctc 4463  
aacacacaca gctcctttca ctctgctg actgccaagc cacctgcac ccccgcccca 4523  
gatctcatga gatcaatcac ttgtatgtct cagcgaactt ggccaccaac acgcctgtcc 4583  
cctgtaactc ctaggggtgc gcctagacag gtacgtctgt tttttatattt aaaagatatg 4643  
ctatgtagat ataagttgag gaagctcacc tcaaaagcct agaatgcagt ttcacagtag 4703  
ctgggatgca tggatgaccc atctcacc cttttttttt ctgcctcaat atcttgatat 4763  
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ctaagtcaaa gaccagtttg acccaaactg gcctttttaa ataatcagga gtgacagagt 5003  
caacttctgc agcacctgct tctcccccac tgtcccttcc atcttggaat gtgtctaaaa 5063  
aagcatagct gccctttgct gtccctcagag tgcatttctt ggagacggca ggcttaggtc 5123  
tactgacag catgccagac acaactgaat cgaagcaggc ctgaagccta ggtcaggggtt 5183  
tcaggagtcc agccccagga ggcaaagtca ccaatgcagg gaggtaaatg ctttttggca 5243  
ggaaaaccaa tagagtttgt tgggtgggga gtcaggggtg ggaggagaag gaggaagagg 5303  
aggaaggcca gactggcctg ccctttctcc catacttcac ccagcagag gttcatggga 5363  
cacagttgga aagccactgg gaggaaatgc ctactacag gggggcctcc tgtagcaagc 5423  
ccagccggtat atcctcctaa tgaaccacaa aggtcaattc acaactgata tcttagctat 5483  
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agtcattttg aaataaaatt aattttacaa 5573

<210> 16  
<211> 842  
<212> PRT  
<213> Homo sapiens

<400> 16  
Met Lys Pro Gly Gly Phe Trp Leu His Leu Thr Leu Leu Gly Ala Ser

1	5	10	15
Leu Pro Ala Ala Leu Gly Trp Met Asp Pro Gly Thr Ser Arg Gly Pro	20	25	30
Asp Val Gly Val Gly Glu Ser Gln Ala Glu Glu Pro Arg Ser Phe Glu	35	40	45
Val Thr Arg Arg Glu Gly Leu Ser Ser His Asn Glu Leu Leu Ala Ser	50	55	60
Cys Gly Lys Lys Phe Cys Ser Arg Gly Ser Arg Cys Val Leu Ser Arg	65	70	75
Lys Thr Gly Glu Pro Glu Cys Gln Cys Leu Glu Ala Cys Arg Pro Ser	85	90	95
Tyr Val Pro Val Cys Gly Ser Asp Gly Arg Phe Tyr Glu Asn His Cys	100	105	110
Lys Leu His Arg Ala Ala Cys Leu Leu Gly Lys Arg Ile Thr Val Ile	115	120	125
His Ser Lys Asp Cys Phe Leu Lys Gly Asp Thr Cys Thr Met Ala Gly	130	135	140
Tyr Ala Arg Leu Lys Asn Val Leu Leu Ala Leu Gln Thr Arg Leu Gln	145	150	155
Pro Leu Gln Glu Gly Asp Ser Arg Gln Asp Pro Ala Ser Gln Lys Arg	165	170	175
Leu Leu Val Glu Ser Leu Phe Arg Asp Leu Asp Ala Asp Gly Asn Gly	180	185	190
His Leu Ser Ser Ser Glu Leu Ala Gln His Val Leu Lys Lys Gln Asp	195	200	205
Leu Asp Glu Asp Leu Leu Gly Cys Ser Pro Gly Asp Leu Leu Arg Phe	210	215	220
Asp Asp Tyr Asn Ser Asp Ser Ser Leu Thr Leu Arg Glu Phe Tyr Met	225	230	235
Ala Phe Gln Val Val Gln Leu Ser Leu Ala Pro Glu Asp Arg Val Ser	245	250	255
Val Thr Thr Val Thr Val Gly Leu Ser Thr Val Leu Thr Cys Ala Val			

[illegible][illegible]





770

775

780

Ala Gln Pro Trp Gly Gly Thr His Arg Ile Met Arg Asp Ser Gly Leu  
785 790 795 800

Phe Gly Gln Tyr Leu Leu Thr Pro Ala Arg Glu Ser Leu Phe Leu Ile  
805 810 815

Asn Gly Arg Gln Asn Thr Leu Arg Cys Glu Val Ser Gly Ile Lys Gly  
820 825 830

Gly Thr Thr Val Val Trp Val Gly Glu Val  
835 840

<210> 17

<211> 5502

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (420)..(2864)

<400> 17

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actagtaacg gccgccagtg tgctggaatt cggcttactc actatagggc tcgagcggct 120

gcccgggcag gtcattaatt ccatttcttt ttagagtatc acagctttct ccttcactga 180

ccaccctttg cttcctgtca gaaagccctg gacagaactc tctgtgggat tctgccccatg 240

tttctgagat atcgctcaa ttgtcctggc tgggctgtcg ggtctgcccg ttttacagat 300

gggcaaaactg gagtgggaag tatccgggtg gcttcctcag gcctgcagct ggtggagcag 360

ctactgaaac aatcaggagc ccagaagctt tgaagtcaca agaagagaag actcccaga 419

atg cag tgt gat gtt ggt gat gga cgc ctg ttt cgc ctt tca ctt aaa 467

Met Gln Cys Asp Val Gly Asp Gly Arg Leu Phe Arg Leu Ser Leu Lys

1

5

10

15

cgt gcc ctt tcc agc tgc cct gac ctc ttt ggg ctt tcc agc cgc aac 515

Arg Ala Leu Ser Ser Cys Pro Asp Leu Phe Gly Leu Ser Ser Arg Asn

20

25

30

gag ctg ctg gcc tcc tgc ggg aag aag ttc tgc agc cga ggg agc cgg 563

[illegible]

Glu Asp Arg Val Ser Val Thr Thr Val Thr Val Gly Leu Ser Thr Val			
225	230	235	240
ctg acc tgc gcc gtc cat gga gac ctg agg cca cca atc atc tgg aag	1187		
Leu Thr Cys Ala Val His Gly Asp Leu Arg Pro Pro Ile Ile Trp Lys			
245	250	255	
cgc aac ggg ctc acc ctg aac ttc ctg gac ttg gaa gac atc aat gac	1235		
Arg Asn Gly Leu Thr Leu Asn Phe Leu Asp Leu Glu Asp Ile Asn Asp			
260	265	270	
ttt gga gag gat gat tcc ctg tac atc acc aag gtg acc acc atc cac	1283		
Phe Gly Glu Asp Asp Ser Leu Tyr Ile Thr Lys Val Thr Thr Ile His			
275	280	285	
atg ggc aat tac acc tgc cat gct tcc ggc cac gag cag ctg ttc cag	1331		
Met Gly Asn Tyr Thr Cys His Ala Ser Gly His Glu Gln Leu Phe Gln			
290	295	300	
acc cac gtc ctg cag gtg aat gtg ccg cca gtc atc cgt gtc tat cca	1379		
Thr His Val Leu Gln Val Asn Val Pro Pro Val Ile Arg Val Tyr Pro			
305	310	315	320
gag agc cag gca cag gag cct gga gtg gca gcc agc cta aga tgc cat	1427		
Glu Ser Gln Ala Gln Glu Pro Gly Val Ala Ala Ser Leu Arg Cys His			
325	330	335	
gct gag ggc att ccc atg ccc aga atc act tgg ctg aaa aac ggc gtg	1475		
Ala Glu Gly Ile Pro Met Pro Arg Ile Thr Trp Leu Lys Asn Gly Val			
340	345	350	
gat gtc tca act cag atg tcc aaa cag ctc tcc ctt tta gcc aat ggg	1523		
Asp Val Ser Thr Gln Met Ser Lys Gln Leu Ser Leu Leu Ala Asn Gly			
355	360	365	
agc gaa ctc cac atc agc agt gtt cgg tat gaa gac aca ggg gca tac	1571		
Ser Glu Leu His Ile Ser Ser Val Arg Tyr Glu Asp Thr Gly Ala Tyr			
370	375	380	
acc tgc att gcc aaa aat gaa gtg ggt gtg gat gaa gat atc tcc tcg	1619		
Thr Cys Ile Ala Lys Asn Glu Val Gly Val Asp Glu Asp Ile Ser Ser			
385	390	395	400
ctc ttc att gaa gac tca gct aga aag acc ctt gca aac atc ctg tgg	1667		
Leu Phe Ile Glu Asp Ser Ala Arg Lys Thr Leu Ala Asn Ile Leu Trp			
405	410	415	
cga gag gaa ggc ctc agc gtg gga aac atg ttc tat gtc ttc tcc gac	1715		

Arg Glu Glu Gly Leu Ser Val Gly Asn Met Phe Tyr Val Phe Ser Asp	
420	425 430
gac ggt atc atc gtc atc cat cct gtg gac tgt gag atc cag agg cac	1763
Asp Gly Ile Ile Val Ile His Pro Val Asp Cys Glu Ile Gln Arg His	
435	440 445
ctc aaa ccc acg gaa aag att ttc atg agc tat gaa gaa atc tgt cct	1811
Leu Lys Pro Thr Glu Lys Ile Phe Met Ser Tyr Glu Glu Ile Cys Pro	
450	455 460
caa aga gaa aaa aat gca acc cag ccc tgc cag tgg gta tct gca gtc	1859
Gln Arg Glu Lys Asn Ala Thr Gln Pro Cys Gln Trp Val Ser Ala Val	
465	470 475 480
aat gtc cgg aac cgg tac atc tat gtg gcc cag cca gca ctg agc aga	1907
Asn Val Arg Asn Arg Tyr Ile Tyr Val Ala Gln Pro Ala Leu Ser Arg	
485	490 495
gtc ctt gtg gtc gac atc caa gcc cag aaa gtc cta cag tcc ata ggt	1955
Val Leu Val Val Asp Ile Gln Ala Gln Lys Val Leu Gln Ser Ile Gly	
500	505 510
gtg gac cct ctg ccg gct aag ctg tcc tat gac aag tca cat gac caa	2003
Val Asp Pro Leu Pro Ala Lys Leu Ser Tyr Asp Lys Ser His Asp Gln	
515	520 525
gtg tgg gtc ctg agc tgg ggg gac gtg cac aag tcc cga cca agt ctc	2051
Val Trp Val Leu Ser Trp Gly Asp Val His Lys Ser Arg Pro Ser Leu	
530	535 540
cag gtg atc aca gaa gcc agc acc ggc cag agc cag cac ctc atc cgc	2099
Gln Val Ile Thr Glu Ala Ser Thr Gly Gln Ser Gln His Leu Ile Arg	
545	550 555 560
aca ccc ttt gca gga gtg gat gat ttc ttc att ccc cca aca aac ctc	2147
Thr Pro Phe Ala Gly Val Asp Asp Phe Phe Ile Pro Pro Thr Asn Leu	
565	570 575
atc atc aac cac atc agg ttt ggc ttc atc ttc aac aag tct gat cct	2195
Ile Ile Asn His Ile Arg Phe Gly Phe Ile Phe Asn Lys Ser Asp Pro	
580	585 590
gca gtc cac aag gtg gac ctg gaa aca atg atg ccc ctc aag acc atc	2243
Ala Val His Lys Val Asp Leu Glu Thr Met Met Pro Leu Lys Thr Ile	
595	600 605
ggc ctg cac cac cat ggc tgc gtg ccc cag gcc atg gca cac acc cac	2291

Gly Leu His His His Gly Cys Val Pro Gln Ala Met Ala His Thr His	
610 615 620	
ctg ggc ggc tac ttc ttc atc cag tgc cga cag gac agc ccc gcc tct	2339
Leu Gly Gly Tyr Phe Phe Ile Gln Cys Arg Gln Asp Ser Pro Ala Ser	
625 630 635 640	
gct gcc cga cag ctg ctc gtt gac agt gtc aca gac tct gtg ctt ggc	2387
Ala Ala Arg Gln Leu Leu Val Asp Ser Val Thr Asp Ser Val Leu Gly	
645 650 655	
ccc aat ggt gat gta aca ggc acc cca cac aca tcc ccc gac ggg cgc	2435
Pro Asn Gly Asp Val Thr Gly Thr Pro His Thr Ser Pro Asp Gly Arg	
660 665 670	
ttc ata gtc agt gct gca gct gac agc ccc tgg ctg cac gtg cag gag	2483
Phe Ile Val Ser Ala Ala Ala Asp Ser Pro Trp Leu His Val Gln Glu	
675 680 685	
atc aca gtg cgg ggc gag atc cag acc ctg tat gac ctg caa ata aac	2531
Ile Thr Val Arg Gly Glu Ile Gln Thr Leu Tyr Asp Leu Gln Ile Asn	
690 695 700	
tgc ggc atc tca gac ttg gcc ttc cag cgc tcc ttc act gaa agc aat	2579
Ser Gly Ile Ser Asp Leu Ala Phe Gln Arg Ser Phe Thr Glu Ser Asn	
705 710 715 720	
caa tac aac atc tac gcg gct ctg cac acg gag ccg gac ctg ctg ttc	2627
Gln Tyr Asn Ile Tyr Ala Ala Leu His Thr Glu Pro Asp Leu Leu Phe	
725 730 735	
ctg gag ctg tcc acg ggg aag gtg ggc atg ctg aag aac tta aag gag	2675
Leu Glu Leu Ser Thr Gly Lys Val Gly Met Leu Lys Asn Leu Lys Glu	
740 745 750	
cca ccc gca ggg cca gct cag ccc tgg ggg ggt acc cac aga atc atg	2723
Pro Pro Ala Gly Pro Ala Gln Pro Trp Gly Gly Thr His Arg Ile Met	
755 760 765	
agg gac agt ggg ctg ttt gga cag tac ctc ctc aca cca gcc cga gag	2771
Arg Asp Ser Gly Leu Phe Gly Gln Tyr Leu Leu Thr Pro Ala Arg Glu	
770 775 780	
tca ctg ttc ctc atc aat ggg aga caa aac acg ctg cgg tgt gag gtg	2819
Ser Leu Phe Leu Ile Asn Gly Arg Gln Asn Thr Leu Arg Cys Glu Val	
785 790 795 800	
tca ggt ata aag ggg ggg acc aca gtg gtg tgg gtg ggt gag gta	2864

Ser Gly Ile Lys Gly Gly Thr Thr Val Val Trp Val Gly Glu Val  
805 810 815

39

gcaagccaca cgggttgagg gaggtggtct caccacagac gtctttgcta atttggccac 4304  
cttcacctac tgacatgacc aggattttcc ttgtccatta aggaatgaac tctttcaagg 4364  
agaggaaacc ctagactctg tgtcactctc aacacacaca gctcctttca ctctgacctg 4424  
actgccaagc cacctgcac ccccgcccca gatctcatga gatcaatcac ttgtatgtct 4484  
cacgcaactt ggtccaccaa acgctgtcc cctgtaactc ctaggggtgc gcctagacag 4544  
gtacgtctgt tttttatttt aaaagatatg ctatgtagat ataagttgag gaagctcacc 4604  
tcaaaagcct agaatgcagt ttcacagtag ctgggatgca tggatgaccc atctcaccac 4664  
tttttttttc ctgcctcaat atcttgatat gttatgttta ctcccaatct cccattttta 4724  
ccactaaaat tctccaactt tcataaactt ttttttggaa aaatttccat tgtatcagcc 4784  
cctgacagaa aaaggatctc tgagcctaaa ggaggaaaag tcccaccaac taccagacca 4844  
gaacacgagc cctctgggc agcaggattc ctaagtcaaa gaccagtttg acccaaactg 4904  
gcctttttaa ataatcagga gtgacagagt caacttctgc agcacctgt tctccccac 4964  
tgtcccttcc atcttggaat gtgtctaaaa aagcatagct gccctttgt gtctcagag 5024  
tgcatttctt ggagacggca ggcttaggtc tctctgacag catgccagac acaactgaat 5084  
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ccaatgcagg gaggtaaatg ccttttggca ggaaaaccaa tagagttggt tgggtgggga 5204  
gtcaggggtg ggaggagaag gaggaagagg aggaaggcca gactggcctg ccctttctcc 5264  
catacttcac cccagcagag gttcatggga cacagttaga aagccactgg gaggaaatgc 5324  
ctcactacag gggggcctcc thtagcaagc ccagccggtat atctctctaa tgaaccaca 5384  
aggtcaattc acaactgata tcttagctat taaagaagta ctgactttac caaagaatc 5444  
atcaagaaag ctatttatat aaacccctc agtcattttg aaataaaatt aattttac 5502

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<210> 18
<211> 815
<212> PRT
<213> Homo sapiens
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**THE UNIVERSITY OF CHICAGO**

Met Gln Cys Asp Val Gly Asp Gly Arg Leu Phe Arg Leu Ser Leu Lys  
1 5 10 15

Arg Ala Leu Ser Ser Cys Pro Asp Leu Phe Gly Leu Ser Ser Arg Asn  
20 25 30

Glu Leu Leu Ala Ser Cys Gly Lys Lys Phe Cys Ser Arg Gly Ser Arg  
35 40 45

Cys Val Leu Ser Arg Lys Thr Gly Glu Pro Glu Cys Gln Cys Leu Glu  
50 55 60

Ala Cys Arg Pro Ser Tyr Val Pro Val Cys Gly Ser Asp Gly Arg Phe  
65 70 75 80

Tyr Glu Asn His Cys Lys Leu His Arg Ala Ala Cys Leu Leu Gly Lys  
85 90 95

Arg Ile Thr Val Ile His Ser Lys Asp Cys Phe Leu Lys Gly Asp Thr  
100 105 110

Cys Thr Met Ala Gly Tyr Ala Arg Leu Lys Asn Val Leu Leu Ala Leu  
115 120 125

Gln Thr Arg Leu Gln Pro Leu Gln Glu Gly Asp Ser Arg Gln Asp Pro  
130 135 140

Ala Ser Gln Lys Arg Leu Leu Val Glu Ser Leu Phe Arg Asp Leu Asp  
145 150 155 160

Ala Asp Gly Asn Gly His Leu Ser Ser Ser Glu Leu Ala Gln His Val  
165 170 175

Leu Lys Lys Gln Asp Leu Asp Glu Asp Leu Leu Gly Cys Ser Pro Gly  
180 185 190

Asp Leu Leu Arg Phe Asp Asp Tyr Asn Ser Asp Ser Ser Leu Thr Leu  
195 200 205

Arg Glu Phe Tyr Met Ala Phe Gln Val Val Gln Leu Ser Leu Ala Pro  
210 215 220

Glu Asp Arg Val Ser Val Thr Thr Val Thr Val Gly Leu Ser Thr Val  
225 230 235 240

Leu Thr Cys Ala Val His Gly Asp Leu Arg Pro Pro Ile Ile Trp Lys

*(Musical notation for Example 6)*

	245		250		255
Arg Asn Gly Leu Thr Leu Asn Phe Leu Asp Leu Glu Asp Ile Asn Asp					
	260		265		270
Phe Gly Glu Asp Asp Ser Leu Tyr Ile Thr Lys Val Thr Thr Ile His					
	275		280		285
Met Gly Asn Tyr Thr Cys His Ala Ser Gly His Glu Gln Leu Phe Gln					
	290		295		300
Thr His Val Leu Gln Val Asn Val Pro Pro Val Ile Arg Val Tyr Pro					
305		310		315	320
Glu Ser Gln Ala Gln Glu Pro Gly Val Ala Ala Ser Leu Arg Cys His					
	325		330		335
Ala Glu Gly Ile Pro Met Pro Arg Ile Thr Trp Leu Lys Asn Gly Val					
	340		345		350
Asp Val Ser Thr Gln Met Ser Lys Gln Leu Ser Leu Leu Ala Asn Gly					
	355		360		365
Ser Glu Leu His Ile Ser Ser Val Arg Tyr Glu Asp Thr Gly Ala Tyr					
	370		375		380
Thr Cys Ile Ala Lys Asn Glu Val Gly Val Asp Glu Asp Ile Ser Ser					
385		390		395	400
Leu Phe Ile Glu Asp Ser Ala Arg Lys Thr Leu Ala Asn Ile Leu Trp					
	405		410		415
Arg Glu Glu Gly Leu Ser Val Gly Asn Met Phe Tyr Val Phe Ser Asp					
	420		425		430
Asp Gly Ile Ile Val Ile His Pro Val Asp Cys Glu Ile Gln Arg His					
	435		440		445
Leu Lys Pro Thr Glu Lys Ile Phe Met Ser Tyr Glu Glu Ile Cys Pro					
	450		455		460
Gln Arg Glu Lys Asn Ala Thr Gln Pro Cys Gln Trp Val Ser Ala Val					
465		470		475	480
Asn Val Arg Asn Arg Tyr Ile Tyr Val Ala Gln Pro Ala Leu Ser Arg					
	485		490		495
Val Leu Val Val Asp Ile Gln Ala Gln Lys Val Leu Gln Ser Ile Gly					

[illegible]

[illegible]

755					760					765					
Arg	Asp	Ser	Gly	Leu	Phe	Gly	Gln	Tyr	Leu	Leu	Thr	Pro	Ala	Arg	Glu
770					775					780					
Ser	Leu	Phe	Leu	Ile	Asn	Gly	Arg	Gln	Asn	Thr	Leu	Arg	Cys	Glu	Val
785					790					795					800
Ser	Gly	Ile	Lys	Gly	Gly	Thr	Thr	Val	Val	Trp	Val	Gly	Glu	Val	
805					810					815					

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<210> 19
<211> 1208
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> (124) .. (1089)
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<400> 19
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gtggccttaat ccgtctccac caccagatct ttctcgtgg attcctctgc taagaccgct 120
gcc atg cca gtg acg gta acc cgc acc acc atc aca acc acc acg acg 168
Met Pro Val Thr Val Thr Arg Thr Thr Ile Thr Thr Thr Thr Thr
1 5 10 15
tca tct tcg ggc ctg ggg tcc ccc atg atc gtg ggg tcc cct cgg gcc 216
Ser Ser Ser Gly Leu Gly Ser Pro Met Ile Val Gly Ser Pro Arg Ala
20 25 30
ctg aca cag ccc ctg ggt ctc ctt cgc ctg ctg cag ctg gtg tct acc 264
Leu Thr Gln Pro Leu Gly Leu Leu Arg Leu Leu Gln Leu Val Ser Thr
35 40 45
tgc gtg gcc ttc tcg ctg gtg gct agc gtg ggc gcc tgg acg ggg tcc 312
Cys Val Ala Phe Ser Leu Val Ala Ser Val Gly Ala Trp Thr Gly Ser
50 55 60
atg ggc aac tgg tcc atg ttc acc tgg tgc ttc tgc ttc tcc gtg acc 360
Met Gly Asn Trp Ser Met Phe Thr Trp Cys Phe Cys Phe Ser Val Thr
65 70 75
ctg atc atc ctc atc gtg gag ctg tgc ggg ctc cag gcc cgc ttc ccc 408
Leu Ile Ile Leu Ile Val Glu Leu Cys Gly Leu Gln Ala Arg Phe Pro

```



80	85	90	95	
ctg tct tgg cgc aac ttc ccc atc acc ttc gcc tgc tat gcg gcc ctc				456
Leu Ser Trp Arg Asn Phe Pro Ile Thr Phe Ala Cys Tyr Ala Ala Leu				
	100	105	110	
ttc tgc ctc tcg gcc tcc atc atc tac ccc acc acc tat gtc cag ttc				504
Phe Cys Leu Ser Ala Ser Ile Ile Tyr Pro Thr Thr Tyr Val Gln Phe				
	115	120	125	
ctg tcc cac ggc cgt tcg cgg gac cac gcc atc gcc gcc acc ttc ttc				552
Leu Ser His Gly Arg Ser Arg Asp His Ala Ile Ala Ala Thr Phe Phe				
	130	135	140	
tcc tgc atc gcg tgt gtg gct tac gcc acc gaa gtg gcc tgg acc cgg				600
Ser Cys Ile Ala Cys Val Ala Tyr Ala Thr Glu Val Ala Trp Thr Arg				
	145	150	155	
gcc cgg ccc ggc gag atc act ggc tat atg gcc acc gta ccc ggg ctg				648
Ala Arg Pro Gly Glu Ile Thr Gly Tyr Met Ala Thr Val Pro Gly Leu				
	160	165	170	175
ctg aag gtg ctg gag acc ttc gtt gcc tgc atc atc ttc gcg ttc atc				696
Leu Lys Val Leu Glu Thr Phe Val Ala Cys Ile Ile Phe Ala Phe Ile				
	180	185	190	
agc gac ccc aac ctg tac cag cac cag ccg gcc ctg gag tgg tgc gtg				744
Ser Asp Pro Asn Leu Tyr Gln His Gln Pro Ala Leu Glu Trp Cys Val				
	195	200	205	
gcg gtg tac gcc atc tgc ttc atc cta gcg gcc atc gcc atc ctg ctg				792
Ala Val Tyr Ala Ile Cys Phe Ile Leu Ala Ala Ile Ala Ile Leu Leu				
	210	215	220	
aac ctg ggg gag tgc acc aac gtg cta ccc atc ccc ttc ccc agc ttc				840
Asn Leu Gly Glu Cys Thr Asn Val Leu Pro Ile Pro Phe Pro Ser Phe				
	225	230	235	
ctg tcg ggg ctg gcc ttg ctg tct gtc ctc ctc tat gcc acc gcc ctt				888
Leu Ser Gly Leu Ala Leu Leu Ser Val Leu Leu Tyr Ala Thr Ala Leu				
	240	245	250	255
gtt ctc tgg ccc ctc tac cag ttc gat gag aag tat ggc ggc cag cct				936
Val Leu Trp Pro Leu Tyr Gln Phe Asp Glu Lys Tyr Gly Gly Gln Pro				
	260	265	270	
cgg cgc tcg aga gat gta agc tgc agc cgc agc cat gcc tac tac gtg				984
Arg Arg Ser Arg Asp Val Ser Cys Ser Arg Ser His Ala Tyr Tyr Val				

[illegible]

275	280	285	
tgt gcc tgg gac cgc cga ctg gct gtg gcc atc ctg acg gcc atc aac			1032
Cys Ala Trp Asp Arg Arg Leu Ala Val Ala Ile Leu Thr Ala Ile Asn			
290	295	300	
cta ctg gcg tat gtg gct gac ctg gtg cac tct gcc cac ctg gtt ttt			1080
Leu Leu Ala Tyr Val Ala Asp Leu Val His Ser Ala His Leu Val Phe			
305	310	315	
gtc aag gtc taagactctc ccaagagggt cccgttccct ctccaacctc			1129
Val Lys Val			
320			
tttgttcttc ttgcccgagt tttctttatg gagtacttct ttctctcgcc tttctctgt			1189
tttctctcttc ctgtctccc			1208

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<210> 20
<211> 322
<212> PRT
<213> Homo sapiens
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<400> 20
Met Pro Val Thr Val Thr Arg Thr Thr Ile Thr Thr Thr Thr Thr Ser
  1                      5                      10                      15
Ser Ser Gly Leu Gly Ser Pro Met Ile Val Gly Ser Pro Arg Ala Leu
      20                      25                      30
Thr Gln Pro Leu Gly Leu Leu Arg Leu Leu Gln Leu Val Ser Thr Cys
      35                      40                      45
Val Ala Phe Ser Leu Val Ala Ser Val Gly Ala Trp Thr Gly Ser Met
      50                      55                      60
Gly Asn Trp Ser Met Phe Thr Trp Cys Phe Cys Phe Ser Val Thr Leu
      65                      70                      75                      80
Ile Ile Leu Ile Val Glu Leu Cys Gly Leu Gln Ala Arg Phe Pro Leu
      85                      90                      95
Ser Trp Arg Asn Phe Pro Ile Thr Phe Ala Cys Tyr Ala Ala Leu Phe
      100                      105                      110
Cys Leu Ser Ala Ser Ile Ile Tyr Pro Thr Thr Tyr Val Gln Phe Leu
      115                      120                      125

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<222> (587) .. (1012)

<400> 21

ggaagaagaa ggaggaggag gagaaggaga agaagaagga gaagaacgca agacttcgtc 60  
tcaaaaaaaaa agaagaaaaa atttaaatac atttaaaaaa gaaggttgca tgctgtggag 120  
caaccagaca attgtgatga aatgtgaagc acaaggcacc agctgtgacg tgtttttgcc 180  
aagaagtcaa accacgttcc aactaaacct ctagagcaaa ctttcatttt cagcaaattc 240  
gaagaaaaga ggaataatgt aaatgacccc acagggaaac agacaaaccc tgaatgtgga 300  
gcatttcaca ggacaaaacc tggacagaca tcggaacact tacaggatgt gtgtagtgtg 360  
gcatgacaga gaactttggg ttcctttaat gtgactgtag acctggcagt gttactataa 420  
gaatcactgg caatcagaca cccgggtgtg ctgagctggc actcagtggg gccggctact 480  
gctcatgtga ttgtggagta gacagttgga agaagtaccc agtccatttg gagagttaaa 540  
actgtgccta acagaggtgt cctctgactt ttcttctgca agctcc atg ttt tca 595  
Met Phe Ser  
1  
cat ctt ccc ttt gac tgt gtc ctg ctg ctg ctg ctg cta cta ctt aca 643  
His Leu Pro Phe Asp Cys Val Leu Leu Leu Leu Leu Leu Leu Thr  
5 10 15  
agg tcc tca gaa gtg gaa tac aga gcg gag gtc ggt cag aat gcc tat 691  
Arg Ser Ser Glu Val Glu Tyr Arg Ala Glu Val Gly Gln Asn Ala Tyr  
20 25 30 35  
ctg ccc tgc ttc tac acc cca gcc gcc cca ggg aac ctc gtg ccc gtc 739  
Leu Pro Cys Phe Tyr Thr Pro Ala Ala Pro Gly Asn Leu Val Pro Val  
40 45 50  
tgc tgg ggc aaa gga gcc tgt cct gtg ttt gaa tgt ggc aac gtg gtg 787  
Cys Trp Gly Lys Gly Ala Cys Pro Val Phe Glu Cys Gly Asn Val Val  
55 60 65  
ctc agg act gat gaa agg gat gtg aat tat tgg aca tcc aga tac tgg 835  
Leu Arg Thr Asp Glu Arg Asp Val Asn Tyr Trp Thr Ser Arg Tyr Trp  
70 75 80  
cta aat ggg gat ttc cgc aaa gga gat gtg tcc ctg acc ata gag aat 883  
Leu Asn Gly Asp Phe Arg Lys Gly Asp Val Ser Leu Thr Ile Glu Asn  
85 90 95



$$\begin{aligned} & \left( \frac{1}{\sqrt{\pi}} e^{-x^2} \right)_{x=0}^{+\infty} = \frac{1}{\sqrt{\pi}} \int_0^{+\infty} e^{-x^2} dx = \frac{1}{\sqrt{\pi}} \cdot \frac{\sqrt{\pi}}{2} = \frac{1}{2}, \\ & \left( \frac{1}{\sqrt{\pi}} e^{-x^2} \right)_{x=-\infty}^0 = \frac{1}{\sqrt{\pi}} \int_{-\infty}^0 e^{-x^2} dx = \frac{1}{\sqrt{\pi}} \cdot \frac{\sqrt{\pi}}{2} = \frac{1}{2}. \end{aligned}$$

ggc ata atg aat gat gaa aaa ttt aac ctg aag ttg gtc atc aaa cca 979  
Gly Ile Met Asn Asp Glu Lys Phe Asn Leu Lys Leu Val Ile Lys Pro  
120 125 130

ggt gag tgg aca ttt gca tgc cat ctt tat gaa taagatttat ctgtggatca 1032  
Gly Glu Trp Thr Phe Ala Cys His Leu Tyr Glu  
135 140

tattaaaggt actgattggt ctcattctctg acttcocctaa ttatagccct ggaggagggc 1092

cactaagacc taaagtttaa caggccccat tggatgatgt cagtgatatt taacaccttc 1152

tctctgtttt aaaactcatg ggtgtgcttg ggcgtgggtgg ctcacacctc t 1203

<210> 22

<211> 142

<212> PRT

<213> Homo sapiens

<400> 22

Met Phe Ser His Leu Pro Phe Asp Cys Val Leu Leu Leu Leu Leu Leu  
1 5 10 15

Leu Leu Thr Arg Ser Ser Glu Val Glu Tyr Arg Ala Glu Val Gly Gln  
20 25 30

Asn Ala Tyr Leu Pro Cys Phe Tyr Thr Pro Ala Ala Pro Gly Asn Leu  
35 40 45

Val Pro Val Cys Trp Gly Lys Gly Ala Cys Pro Val Phe Glu Cys Gly  
50 55 60

Asn Val Val Leu Arg Thr Asp Glu Arg Asp Val Asn Tyr Trp Thr Ser  
65 70 75 80

Arg Tyr Trp Leu Asn Gly Asp Phe Arg Lys Gly Asp Val Ser Leu Thr  
85 90 95

Ile Glu Asn Val Thr Leu Ala Asp Ser Gly Ile Tyr Cys Cys Arg Ile  
100 105 110

Gln Ile Pro Gly Ile Met Asn Asp Glu Lys Phe Asn Leu Lys Leu Val



[illegible]

cag gtc tgg cta agg tac cag aag cca aca agt ccc aga aag gtc aag 769  
Gln Val Trp Leu Arg Tyr Gln Lys Pro Thr Ser Pro Arg Lys Val Lys  
80 85 90

tgactttccc aaggtcacac agcaagttga tggcagagct ggggtacagga ctcaga 825

```
<210> 24
<211> 92
<212> PRT
<213> Homo sapiens
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<400> 24  
Met Asp Ile Lys Ala Val Ser Pro Ser Ser Pro Ala Thr Thr Asp Ser  
1 5 10 15

Thr Ala Gly Thr Val Leu Leu Cys Phe Phe Lys Ala Trp Val Leu Gln  
20 25 30

Lys Gln Leu Leu Ser Cys Thr Pro Lys Val Glu Trp Lys Ser Leu Gly

Lys Gly Gly Gly Glu Ser Val Lys Gly Met Ala Arg Arg Gly Gly Arg  
50 55 60

Gln Gly Thr Gly Val Leu Ala Thr Ala Asp Gly Lys Gln Val Trp Leu  
65 70 75 80

Arg Tyr Gln Lys Pro Thr Ser Pro Arg Lys Val Lys  
85 90

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<210> 25
<211> 1099
<212> DNA
<213> Homo sapiens
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<220>  
<221> CDS  
<222> (83) .. (889)
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<400> 25  
ctagaattca qcqgccgctg aattctagtg cagagtgaac aaggccgcc tcattcagct 60

tctctctgag agccagggcc ac atg gct cac ctg gtg aac tcc gtc agc gac	112
Met Ala His Leu Val Asn Ser Val Ser Asp	
1 5 10	
atc ctg gat gcc ctg cag agg gac cgg ggg ctg ggc cgg ccc cgc aac	160
Ile Leu Asp Ala Leu Gln Arg Asp Arg Gly Leu Gly Arg Pro Arg Asn	
15 20 25	
aag gcc gac ctt cag aga gcg cct gcc cgg gga acc cgg ccc cgg ggc	208
Lys Ala Asp Leu Gln Arg Ala Pro Ala Arg Gly Thr Arg Pro Arg Gly	
30 35 40	
tgt gcc act ggc tcc cgg ccc cga gac tgt ctg gac gtc ctc cta agc	256
Cys Ala Thr Gly Ser Arg Pro Arg Asp Cys Leu Asp Val Leu Leu Ser	
45 50 55	
gga cag cag gac gat ggc gtc tac tct gtc ttt ccc acc cac tac ccg	304
Gly Gln Gln Asp Asp Gly Val Tyr Ser Val Phe Pro Thr His Tyr Pro	
60 65 70	
gcc ggc ttc cag gtg tac tgt gac atg cgc acg gac ggc ggc ggc tgg	352
Ala Gly Phe Gln Val Tyr Cys Asp Met Arg Thr Asp Gly Gly Gly Trp	
75 80 85 90	
acg gtg ttt cag cgc cgg gag gac ggc tcc gtg aac ttc ttc cgg ggc	400
Thr Val Phe Gln Arg Arg Glu Asp Gly Ser Val Asn Phe Phe Arg Gly	
95 100 105	
tgg gat gcg tac cga gac ggc ttt ggc agg ctc acc ggg gag cac tgg	448
Trp Asp Ala Tyr Arg Asp Gly Phe Gly Arg Leu Thr Gly Glu His Trp	
110 115 120	
cta ggg ctc aag agg atc cac gcc ctg acc aca cag gct gcc tac gag	496
Leu Gly Leu Lys Arg Ile His Ala Leu Thr Thr Gln Ala Ala Tyr Glu	
125 130 135	
ctg cac gtg gac ctg gag gac ttt gag aat ggc acg gcc tat gcc cgc	544
Leu His Val Asp Leu Glu Asp Phe Glu Asn Gly Thr Ala Tyr Ala Arg	
140 145 150	
tac ggg agc ttc ggc gtg ggc ttg ttc tcc gtg gac cct gag gaa gac	592
Tyr Gly Ser Phe Gly Val Gly Leu Phe Ser Val Asp Pro Glu Glu Asp	
155 160 165 170	
ggg tac ccg ctc acc gtg gct gac tat tcc ggc act gca ggc gac tcc	640
Gly Tyr Pro Leu Thr Val Ala Asp Tyr Ser Gly Thr Ala Gly Asp Ser	
175 180 185	

ctc ctg aag cac agc ggc atg agg ttc acc acc aag gac cgt gac agc 688  
Leu Leu Lys His Ser Gly Met Arg Phe Thr Thr Lys Asp Arg Asp Ser  
190 195 200

gac cat tca gag aac aac tgt gcc gcc ttc tac cgc ggt gcc tgg tgg 736  
Asp His Ser Glu Asn Asn Cys Ala Ala Phe Tyr Arg Gly Ala Trp Trp  
205 210 215

tac cgc aac tgc cac acg tcc aac ctc aat ggg cag tac ctg cgc ggt 784  
Tyr Arg Asn Cys His Thr Ser Asn Leu Asn Gly Gln Tyr Leu Arg Gly  
220 225 230

gcg cac gcc tcc tat gcc gac ggc gtg gag tgg tcc tcc tgg acc ggc 832  
Ala His Ala Ser Tyr Ala Asp Gly Val Glu Trp Ser Ser Trp Thr Gly  
235 240 245 250

tgg cag tac tca ctc aag ttc tct gag atg aag atc cgg ccg gtc cgg 880  
 Trp Gln Tyr Ser Leu Lys Phe Ser Glu Met Lys Ile Arg Pro Val Arg  
 255 260 265

gag gac cgc tagaccggtg caccttgtcc ttggccctgc tggtcctgt 929  
Glu Asp Arg

cqccccatcc ccgacccccac ctcactcttt cgtgaatggt ctccacccac ctgtgcctgg 989

cggacccact ctccagtagg gaggggcccgg gccatccctg acacgaagct ccttggggccg 1049

gtgaagtcac acatcgccctt ctcgccgtcc ccaccccctc catttggcag 1099

```
<210> 26
<211> 269
<212> PRT
<213> Homo sapiens
```

```
<400> 26
Met Ala His Leu Val Asn Ser Val Ser Asp Ile Leu Asp Ala Leu Gln
      1              5              10              15
```

Arg Asp Arg Gly Leu Gly Arg Pro Arg Asn Lys Ala Asp Leu Gln Arg  
20 25 30

Ala Pro Ala Arg Gly Thr Arg Pro Arg Gly Cys Ala Thr Gly Ser Arg  
35 40 45

Pro Arg Asp Cys Leu Asp Val Leu Leu Ser Gly Gln Gln Asp Asp Gly  
50 55 60





[illegible]

gca ggc gac tcc ctc ctg aag cac agc ggc atg agg ttc acc acc aag 631  
Ala Gly Asp Ser Leu Leu Lys His Ser Gly Met Arg Phe Thr Thr Lys  
185 190 195

gac cgt gac agc gac cat tca gag aac aac tgt gcc gcc ttc tac cgc 679  
Asp Arg Asp Ser Asp His Ser Glu Asn Asn Cys Ala Ala Phe Tyr Arg  
200 205 210

ggt gcc tgg tgg tac cgc aac tgc cac acg tcc aac ctc aat ggg cag 727  
Gly Ala Trp Trp Tyr Arg Asn Cys His Thr Ser Asn Leu Asn Gly Gln  
215 220 225 230

tac ctg cgc ggt gcg cac gcc tcc tat gcc gac ggc gtg gag tgg tcc 775  
Tyr Leu Arg Gly Ala His Ala Ser Tyr Ala Asp Gly Val Glu Trp Ser  
235 240 245

tcc tgg acc ggc tgg cag tac tca ctc aag ttc tct gag atg aag atc 823  
Ser Trp Thr Gly Trp Gln Tyr Ser Leu Lys Phe Ser Glu Met Lys Ile  
250 255 260

cgg ccg gtc cgg gag gac cgc tagaccggtg caccttgtcc ttggcctgc 874  
 Arg Pro Val Arg Glu Asp Arg  
 265

tggtccctgt cgccccatcc cegacccac ctcactcttt cgtgaatggt ctccacccac 934

ctgtgacctgg cggaccact ctccagtagg gaggggcccgg gccatccctg acacgaagct 994

ccctgggccg gtgaagtcac acatcgccctt ctgcgcgtcc ccaccccctc catttggcag 1054

<210> 28

<211> 269

<212> PRT

<213> Homo sapiens

<400> 28

Met Ala His Leu Val Asn Ser Val Ser Asp Ile Leu Asp Ala Leu Gln  
1 5 10 15

Arg Asp Arg Gly Leu Gly Arg Pro Arg Asn Lys Ala Asp Leu Gln Arg  
20 25 30

Ala Pro Ala Arg Gly Thr Arg Pro Arg Gly Cys Ala Thr Gly Ser Arg  
35 40 45



Pro Arg Asp Cys Leu Asp Val Leu Leu Ser Gly Gln Gln Asp Asp Gly  
50 55 60

Val Tyr Ser Val Phe Pro Thr His Tyr Pro Ala Gly Phe Gln Val Tyr  
65 70 75 80

Cys Asp Met Arg Thr Asp Gly Gly Gly Trp Thr Val Phe Gln Arg Arg  
85 90 95

Glu Asp Gly Ser Val Asn Phe Phe Arg Gly Trp Asp Ala Tyr Arg Asp  
100 105 110

Gly Phe Gly Arg Leu Thr Gly Glu His Trp Leu Gly Leu Lys Arg Ile  
115 120 125

His Ala Leu Thr Thr Gln Ala Ala Tyr Glu Leu His Val Asp Leu Glu  
130 135 140

Asp Phe Glu Asn Gly Thr Ala Tyr Ala Arg Tyr Gly Ser Phe Gly Val  
145 150 155 160

Gly Leu Phe Ala Val Asp Pro Glu Glu Asp Gly His Pro Leu Thr Val  
165 170 175

Ala Asp Tyr Ser Gly Thr Ala Gly Asp Ser Leu Leu Lys His Ser Gly  
180 185 190

Met Arg Phe Thr Thr Lys Asp Arg Asp Ser Asp His Ser Glu Asn Asn  
195 200 205

Cys Ala Ala Phe Tyr Arg Gly Ala Trp Trp Tyr Arg Asn Cys His Thr  
210 215 220

Ser Asn Leu Asn Gly Gln Tyr Leu Arg Gly Ala His Ala Ser Tyr Ala  
225 230 235 240

Asp Gly Val Glu Trp Ser Ser Trp Thr Gly Trp Gln Tyr Ser Leu Lys  
245 250 255

Phe Ser Glu Met Lys Ile Arg Pro Val Arg Glu Asp Arg  
260 265

<210> 29  
<211> 498  
<212> DNA  
<213> Homo sapiens

[illegible]

<222> (1) .. (498)

[illegible]



cagagagcgc	ctgcccgggg	aacccgggcc	cggggctgtg	ccactggctc	ccggccccga	60
gactgtcttg	acgtcctcct	aagcggacag	caggacgatg	gcgtctactc	tgtctttccc	120
acccactacc	cggccggctt	ccaggtgtac	tgtgacatgc	gcacggacgg	cggcggctgg	180
acggtgtttc	agcgccggga	ggacggctcc	gtgaacttct	tccggggctg	ggacgcgtac	240
cgagacggct	ttggcaggct	caccggggag	cactggctag	ggctcaagag	gatccacgcc	300
ctgaccacac	aggtgccta	cgagctgcac	gtggacctgg	aggactttga	gaatggcacg	360
gcctatgccc	gctacgggag	cttcggcgctg	ggcttgttcg	ccgtggaccc	tgaggaagac	420
gggtaccgcg	tcaccgtggc	tgactattcc	ggcactgcag	gcgactccct	cctgaagcac	480
agcggcatga	ggttcaccac	caaggaccgt	gacagcgacc	attcagagaa	caactgtgcc	540
gccttctacc	gcggtgcctg	gtggtaccgc	aactgccaca	cgtccaacct	caatgggcag	600
tacctgcgcg	gtg'gcacgc	ctcctatgcc	gacggcgctg	agtggctctc	ctggaccggc	660
tggcagtact	cactcaagtt	ctctgagatg	aagatccggc	cggtccggga	ggaccgc	717

<210> 32

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oligo Primer

<400> 32

ctcgtcctcg agggtaagcc tatccctaac

30

<210> 33

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oligo Primer

<400> 33

ctcgtcgggc ccctgatcag cgggtttaaa c

31

<210> 34  
 <211> 40  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Oligo Primer

<400> 34  
 ctcgtcagat ctcgcagcgg agatgccacc ttccccaag 40

<210> 35  
 <211> 40  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Oligo Primer

<400> 35  
 ctcgtcctcg agcctcctcg acgtgccgtt gctcacctcg 40

<210> 36  
 <211> 43  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Oligo Primer

<400> 36  
 ggatccacca tgaattttct gaaattaatt gctgtgttta tag 43

<210> 37  
 <211> 36  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Oligo Primer

<400> 37  
 ctcgagattc agcagctcca gactccccca tccatg 36

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<210> 38

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oligo Primer

<400> 38

agatctcaga gagcgccctgc ccgggggaacc

30

<210> 39

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oligo Primer

<400> 39

ctcgaggcgg tcctcccgga ccggccggat c

31

<210> 40

<211> 18

<212> DNA

### <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oligo Primer

<400> 40

gaggacggct ccgtgaac

18

<210> 41

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oligo Primer

<400> 41

gttcacggag ccgtcctc

18



<210> 46  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oligo Primer

<400> 46

tccctgggaa atgtcacaca

20

<210> 47

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oligo Primer

<400> 47

ttcctgggtgc caaagaatga g

21

<210> 48

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oligo Primer

<400> 48

agaacatcaa tcttccttcc ccactcctga g

31

<210> 49

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oligo Primer

<400> 49

gcctggctct ctggatagac a

21





<210> 54  
 <211> 31  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Oligo Primer

<400> 54  
 cctctttgtt cttcttgccc gagttttctt t 31

<210> 55  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Oligo Primer

<400> 55  
 tggaagtcctc tcggtaaagg a 21

<210> 56  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Oligo Primer

<400> 56  
 aggacacctg tgccctgtct 20

<210> 57  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Oligo Primer

<400> 57  
 cccgccttgc cattcccttc a 21